Figure 1

Vezf1: 1 to 3640

```
CGGGGGGAGTGGGGAGGAGGGGGGTCGGCCGCCGCAGCCATGGAGGCCAACTGGACCGCGTTCCTGTTCCAGGCCCACGAAGCATCCCAT      90
                                                M  E  A  N  W  T  A  F  L  F  Q  A  H  E  A  S  H  17

CACCAACAGCAGGCAGCGCAGAACAGCTTGCTGCCCCTCCTGAGTTCTGCTGTGGAGCCCCCTGATCAGAAACCGTTGCTTCCAATACCA      180
H  Q  Q  Q  A  A  Q  N  S  L  L  P  L  L  S  S  A  V  E  P  P  D  Q  K  P  L  L  P  I  P  47

ATTACTCAGAAACCTCAGGCTGCACCAGAAACATTAAAGGATGCCATTGGGATTAAAAAAGAAAAACCCAAAACTTCGTTTGTGTGCACT      270
I  T  Q  K  P  Q  A  A  P  E  T  L  K  D  A  I  G  I  K  K  E  K  P  K  T  S  F  V  C  T  77

TACTGCAGTAAAGCATTCAGGGACAGCTATCACCTGAGGCGCCATCAGTCCTGCCACACAGGGATCAAGTTGGTGTCTCGGGCAAAGAAA      360
Y  C  S  K  A  F  R  D  S  Y  H  L  R  R  H  Q  S  C  H  T  G  I  K  L  V  S  R  A  K  K  107

ACCCCCACCACGGTGGTTCCCCTTATCTCCACCATTGCTGGGGACAGCAGCCGAACTTCGTTGGTTTCAACTATTGCAGGCATCTTGTCA      450
T  P  T  T  V  V  P  L  I  S  T  I  A  G  D  S  S  R  T  S  L  V  S  T  I  A  G  I  L  S  137

ACAGTCACTACATCTTCCTCGGGCACCAACCCCAGCAGCAGCGCTAGTACCACAGCAATGCCTGTGCCCCAGTCTGTCAAGAAACCCAGT      540
T  V  T  T  S  S  S  G  T  N  P  S  S  S  A  S  T  T  A  M  P  V  P  Q  S  V  K  K  P  S  167

AAGCCTGTCAAGAAGAACCACGCCTGTGAGATGTGTGGGAAGGCCTTCCGGGATGTGTACCACCTCAATCGGCACAAGCTCTCCCATTCG      630
K  P  V  K  K  N  H  A  C  E  M  C  G  K  A  F  R  D  V  Y  H  L  N  R  H  K  L  S  H  S  197

GACGAAAAGCCCTTTGAGTGTCCTATTTGTAATCAGCGCTTCAAGAGGAAGGACCGGATGACTTACCATGTGAGGTCTCATGAAGGAGGC      720
D  E  K  P  F  E  C  P  I  C  N  Q  R  F  K  R  K  D  R  M  T  Y  H  V  R  S  H  E  G  G  227

ATCACCAAACCCTATACTTGCAGTGTTTGTGGGAAAGGCTTCTCAAGGCCTGACCACCTAAGCTGTCATGTAAAACATGTGCATTCAACA      810
I  T  K  P  Y  T  C  S  V  C  G  K  G  F  S  R  P  D  H  L  S  C  H  V  K  H  V  H  S  T  257

GAAAGACCCTTCAAATGCCAAACGTGCACTGCTGCCTTTGCCACCAAAGACAGACTACGGACACACATGGTGCGCCACGAAGGCAAGGTA      900
E  R  P  F  K  C  Q  T  C  T  A  A  F  A  T  K  D  R  L  R  T  H  M  V  R  H  E  G  K  V  287

TCATGTAACATCTGTGGGAAGCTCTTGAGTGCAGCATATATCACCAGCCACTTAAAGACACATGGGCAGAGCCAAAGTATCAACTGTAAC      990
S  C  N  I  C  G  K  L  L  S  A  A  Y  I  T  S  H  L  K  T  H  G  Q  S  Q  S  I  N  C  N  317

ACGTGCAAACAAGGCATCAGCAAAACGTGCATGAGTGAGGAGACCAGCAATCAGAAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAG     1080
T  C  K  Q  G  I  S  K  T  C  M  S  E  E  T  S  N  Q  K  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  347
                                                   *     *  *  *  *  *  *  *  *  *  *  *

CAACAACAACAACATGTGACAAGCTGGCCAGGGAAGCAGGTAGAGACACTGAGACTGTGGGAAGAAGCTGTCAAAGCAAGAAAGAAAGAA     1170
Q  Q  Q  Q  H  V  T  S  W  P  G  K  Q  V  E  T  L  R  L  W  E  E  A  V  K  A  R  K  K  E  377
*  *  *  *

GCTGCCAACCTGTGCCAAACCTCCACGGCTGCTACGACACCAGTGACTCTCACTACTCCATTCAATATAACGTCCTCTGTGTCGTCTGGG     1260
A  A  N  L  C  Q  T  S  T  A  A  T  T  P  V  T  L  T  T  P  F  N  I  T  S  S  V  S  S  G  407

ACTATGTCAAACCCAGTCACAGTGGCAGCTGCAATGAGCATGAGAAGTCCAGTAAATGTCTCAAGTGCAGTTAACATAACCAGCCCCTTA     1350
T  M  S  N  P  V  T  V  A  A  A  M  S  M  R  S  P  V  N  V  S  S  A  V  N  I  T  S  P  L  437

GCCATGACCTCACCTTTAACACTCACCACCCCAGTCAACCTCCCCACCCCTGTGACCGCCCCAGTGAATATAGCACACCCTGTCACCATC     1440
A  M  T  S  P  L  T  L  T  T  P  V  N  L  P  T  P  V  T  A  P  V  N  I  A  H  P  V  T  I  467

ACATCTCCAATGAACCTGCCCACTCCTATGACATTAGCTGCCCCTCTCAATATAGCAATGAGGCCTGTAGAAAGTATGCCTTTCTTGCCC     1530
T  S  P  M  N  L  P  T  P  M  T  L  A  A  P  L  N  I  A  M  R  P  V  E  S  M  P  F  L  P  497

CAAGCTTTGCCTACGTCACCGCCTTGGTAAACAGTATTATAAGTCAAAATTGGGTTAAAGTAAATATTTACCAGCAACTTAACCTTAGTT     1620
Q  A  L  P  T  S  P  P  W                                                                  506

GATTAAAGCAAAAAGCAGACTATGAAATTGGGAGGTTTTATTATGTTAGTTAATAAGAGTGTAGTAGCTCCAATTTTGCTGGGGTTGTTC     1710
AAAGTAGGGTATATGTGTAACTTATCACTGGACCACTTTAGTTTACTCAGAAACCCCTTTAGCTGACACCATTGCTTAAACAGGATAGTA     1800
GCTGGCAAGACGAAATGCCAGAATTAAAACCAATCATAAAACCCATTTCAAAATAAAAAAGCATTATTTGTTTTTATTATTATTTTTAAT     1890
ACAACAGAATCATTTTATTGTAAACACTAGCAGAGTTCTTCCCTCTGTACAAGGTGGACGGTTTTAACCTGGAGCTCAAGCCCACAGACT     1980
GAGAGCTAGTGTAGCATTGTCTGTGGTTTTGCTCGTATGAGTGAACAGAGGCATTGTCATAATAAAATGCATTTCAGAGAATATGCATTT     2070
TACCTTTGGGAATATGTTAATTTCAGGCAGCATTCCCTATGGGAAAGGTGATACCAGCTCTGATATGCAAAGCATATGATAATTTATCAT     2160
TCTAACTTCAACATATAATAGGGATTGTGACCTGATATTTGGAGATGTAAATATTGCTCAGCATATTAATCCCTGATGGAATATAGCATT     2250
GTAGTTGACTTTTTAAAAAAAAAAAAAACAAAAAAAAAAAAAAAGGAATTCCGAGAGCTGTCACTGCCTTTGAATGCTATCCCTGGGATAGG     2340
GGTGGCTTCAGAACCCAGGAAGTGGCCAAGGGGCACAGACTCTGCTGGAGGCCTGAGCCGGGGGTTCCATAGGAGACTGACAGGAGACAT     2430
TTTGCCTTAGGCCACAAAAAGAAGAAGGCTACCCCACTTACAGATGCAGACCATGTGGGGCTCCGGAGAACTGCTTGTAGCATGGTTTCT     2520
AGTGTTGGCAGCAGATGGTACTACTGAGCATGTCTACAGACCCAGTCGTAGAGTGTGTACTGTGGGGATTTCCGGAGGTTCCATCTCGGA     2610
GACCTTTGTGCAGCGTGTATACCAGCCTTACCTCACCACTTGCGACGGACACAGAGCCTGCAGCACCTACCGAACCATCTACCGGACTGC     2700
CTATCGCCGTAGCCCTGGGGTGACTCCCGCAAGGCCTCGCTATGCTTGCTGCCCTGGTTGGAAGAGGACCAGTGGGCTCCCTGGGGCTTG     2790
TGGAGCAGCAATATGCCAGCCTCCATGTGGGAATGGAGGGAGTTCATCCGCCCAGGACACTGCCGCTGCCCTGTGGATGGCAGGGAGATA     2880
CTTGCCAGACAGATGTTGATGAATGCAGTACAGGAGAGGCCAGTTGTCCCCAGCGCTGTGTCAATACTGTGGGAAGTTACTGGTGCCAGG     2970
GATGGGAGGGACAAAGCCCATCTGCAGATGGGACCCCCTGCCTGTCTAAGGAGGGGCCCTCCCCTTTCCCCCCAAACCCCACAGCAGGAG     3060
TGGACAGCATGGCGAGAGAGGAGGTGTACAGGCTGCAGGCTCGGGTTGATGTGCTAGAACAGAAACTGCAGTTGGTGCTGGCCCCACTGC     3150
ACAGCCTGGCCTCTCGGTCCACAGAGCATGGGCTACAAGATCCTGGCAGCCTGCTGGTGTCCTTCTTGGAGGAACATCTGGGGTCCTGTG     3240
AGTCCCACAAGACACCACTCCACCCACAGAGAGCCTAGGGGACCCATGGGGTGGACACCAGGGCTGGGTGGATGGAACTTCTTCTGGGAT     3330
GGGCAGATTTGCAAGTTTACACCTTTTTTCCTCTCCTGCCCTAGGCTCCTGCAAAAAAGATCTGTGATAACCTCTCACCACCAGGCTGGA     3420
TAGAGCAGTATCCAGATCCCTTGTAGCCAGAGTTCAGGGACGCTGTCTGGTGGTGCCTATGAGCAGAAGCCCTGCCTCATTGTCCCTCTT     3510
TCTTAGGAGGTTCCTAGGACTTGGGTATGGGGAGTGGGGTCTTGTGTGACTCTTCAGTGGGGCTCCCTGTCTAAGTGGTAAGGTGGGGAT     3600
TGTCTCCATCTTTGTCATAATAAAGCTGAGACTTGAAAAAAAAAA                                               3645
```

Figure 2

Human DB1 DNA and Protein S q nc s:

```
         10         20         30         40         50         60
AGCGGGGGGAGTGGGGAGGAGGGGGGTCGGCCGCCGCAGCCATGGAGGCCAACTGGACCG
                                                M  E  A  N  W  T>

         70         80         90        100        110        120
CGTTCCTGTTCCAGGCCCATGAAGCTTCCCATCACCAACAGCAGGCAGCACAGAACAGCT
A  F  L  F  Q  A  H  E  A  S  H  H  Q  Q  Q  A  A  Q  N  S>

        130        140        150        160        170        180
TGCTGCCCCTCCTGAGCTCTGCCGTGGAGCCCCCTGATCAGAAACCATTGCTTCCAATAC
L  L  P  L  L  S  S  A  V  E  P  P  D  Q  K  P  L  L  P  I>

        190        200        210        220        230        240
CAATAACTCAGAAACCTCAGGGTGCACCAGAAACATTAAAGGATGCCATTGGGATTAAAA
P  I  T  Q  K  P  Q  G  A  P  E  T  L  K  D  A  I  G  I  K>

        250        260        270        280        290        300
AAGAAAAACCCAAAACTTCATTTGTGTGCACTTACTGCAGTAAAGCTTTCAGGGACAGCT
K  E  K  P  K  T  S  F  V  C  T  Y  C  S  K  A  F  R  D  S>

        310        320        330        340        350        360
ATCACCTGAGGCGCCACGAATCCTGCCACACAGGGATCAAGTTGGTGTCCCGGCCAAAGA
Y  H  L  R  R  H  E  S  C  H  T  G  I  K  L  V  S  R  P  K>

        370        380        390        400        410        420
AAACCCCCACCACGGTGGTTCCCCTTATCTCTACCATCGCTGGGGACAGCAGCCGAACTT
K  T  P  T  T  V  V  P  L  I  S  T  I  A  G  D  S  S  R  T>

        430        440        450        460        470        480
CGTTGGTCTCGACCATTGCAGGCATCTTGTCAACAGTCACTACATCTTCCTCGGGCACCA
S  L  V  S  T  I  A  G  I  L  S  T  V  T  T  S  S  S  G  T>

        490        500        510        520        530        540
ACCCCAGTAGCAGTGCCAGCACCACAGCTATGCCAGTGACCCAGTCTGTCAAGAAACCCA
N  P  S  S  S  A  S  T  T  A  M  P  V  T  Q  S  V  K  K  P>

        550        560        570        580        590        600
GTAAGCCTGTCAAGAAGAACCATGCTTGTGAGATGTGTGGGAAGGCCTTCCGAGATGTGT
S  K  P  V  K  K  N  H  A  C  E  M  C  G  K  A  F  R  D  V>

        610        620        630        640        650        660
ACCATCTCAATCGACACAAGCTCTCCCATTCAGATGAGAAACCCTTTGAGTGTCCTATTT
Y  H  L  N  R  H  K  L  S  H  S  D  E  K  P  F  E  C  P  I>

        670        680        690        700        710        720
GTAATCAGCGCTTCAAGAGGAAGGACCGGATGACTTACCATGTGAGGTCTCATGAAGGAG
C  N  Q  R  F  K  R  K  D  R  M  T  Y  H  V  R  S  H  E  G>

        730        740        750        760        770        780
GCATCACCAAACCCTATACTTGCAGTGTTTGTGGGAAAGGCTTCTCAAGGCCTGACCACT
G  I  T  K  P  Y  T  C  S  V  C  G  K  G  F  S  R  P  D  H>
```

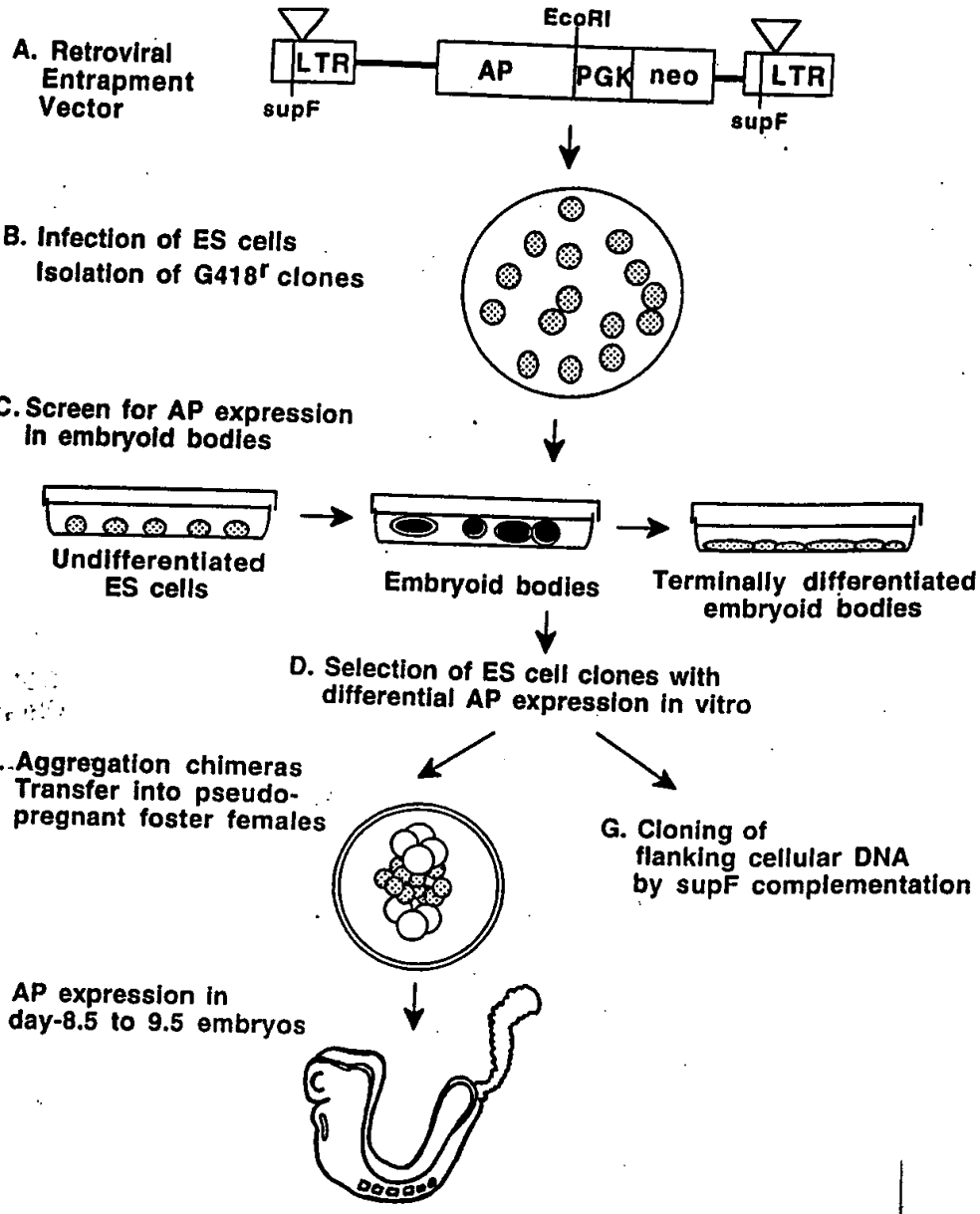
Figure 2 (con't)

```
        790        800        810        820        830        840
TAAGCTGTCATGTAAAACATGTCCATTCAACAGAAAGACCCTTCAAATGCCAAACGTGCA
L  S  C  H  V  K  H  V  H  S  T  E  R  P  F  K  C  Q  T  C>

        850        860        870        880        890        900
CTGCTGCCTTTGCCACCAAAGACAGACTGCGGACACACATGGTGCGCCATGAAGGCAAGG
T  A  A  F  A  T  K  D  R  L  R  T  H  M  V  R  H  E  G  K>

        910        920        930        940        950        960
TATCATGTAACATCTGTGGGAAGCTCCTGAGTGCAGCATACATCACCAGCCACTTAAAGA
V  S  C  N  I  C  G  K  L  L  S  A  A  Y  I  T  S  H  L  K>

        970        980        990       1000       1010       1020
CTCATGGGCAGAGCCAAAGTATCAACTGTAATACATGTAAACAAGGCATCAGTAAAACAT
T  H  G  Q  S  Q  S  I  N  C  N  T  C  K  Q  G  I  S  K  T>

       1030       1040       1050       1060       1070       1080
GCATGAGTGAAGAGACCAGTAACCAAAAGCAGCAGCAGCAGCAGCAGCAACAACAAC
C  M  S  E  E  T  S  N  Q  K  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q>

       1090       1100       1110       1120       1130       1140
AACAACAACATGTGACAAGCTGGCCAGGGAAGCAAGTAGAAACACTCAGACTGTGGGAAG
Q  Q  Q  H  V  T  S  W  P  G  K  Q  V  E  T  L  R  L  W  E>

       1150       1160       1170       1180       1190       1200
AAGCTGTTAAAGCAAGGAAGAAAGAAGCTGCTAACCTGTGCCAAACCTCCACGGCTGCTA
E  A  V  K  A  R  K  K  E  A  A  N  L  C  Q  T  S  T  A  A>

       1210       1220       1230       1240       1250       1260
CGACACCTGTGACTCTCACTACTCCATTCAGTATAACATCCTCTGTGTCGTCTGAGACTA
T  T  P  V  T  L  T  T  P  F  S  I  T  S  S  V  S  S  E  T>

       1270       1280       1290       1300       1310       1320
TGTCAAACCCAGTCACAGTGGCAGCTGCAATGAGCATGAGAAGTCCAGTAAATGTTTCAA
M  S  N  P  V  T  V  A  A  A  M  S  M  R  S  P  V  N  V  S>

       1330       1340       1350       1360       1370       1380
GTGCAGTTAACATAACCAGCCCAATGAACATAGGGCATCCTGTAACTATAACCAGTCCAT
S  A  V  N  I  T  S  P  M  N  I  G  H  P  V  T  I  T  S  P>

       1390       1400       1410       1420       1430       1440
TATCCATGACCTCTCCTTTAACACTCACTACCCCAGTCAACCTCCCCACCCCCGTCACTG
L  S  M  T  S  P  L  T  L  T  T  P  V  N  L  P  T  P  V  T>

       1450       1460       1470       1480       1490       1500
CCCCAGTGAATATAGCACACCCTGTCACCATCACATCTCCAATGAATCTACCCACACCTA
A  P  V  N  I  A  H  P  V  T  I  T  S  P  M  N  L  P  T  P>

       1510       1520       1530       1540       1550       1560
TGACATTAGCCGCCCCTCTCAATATAGCAATGAGACCTGTAGAGAGCATGCCTTTCTTGC
M  T  L  A  A  P  L  N  I  A  M  R  P  V  E  S  M  P  F  L>
```

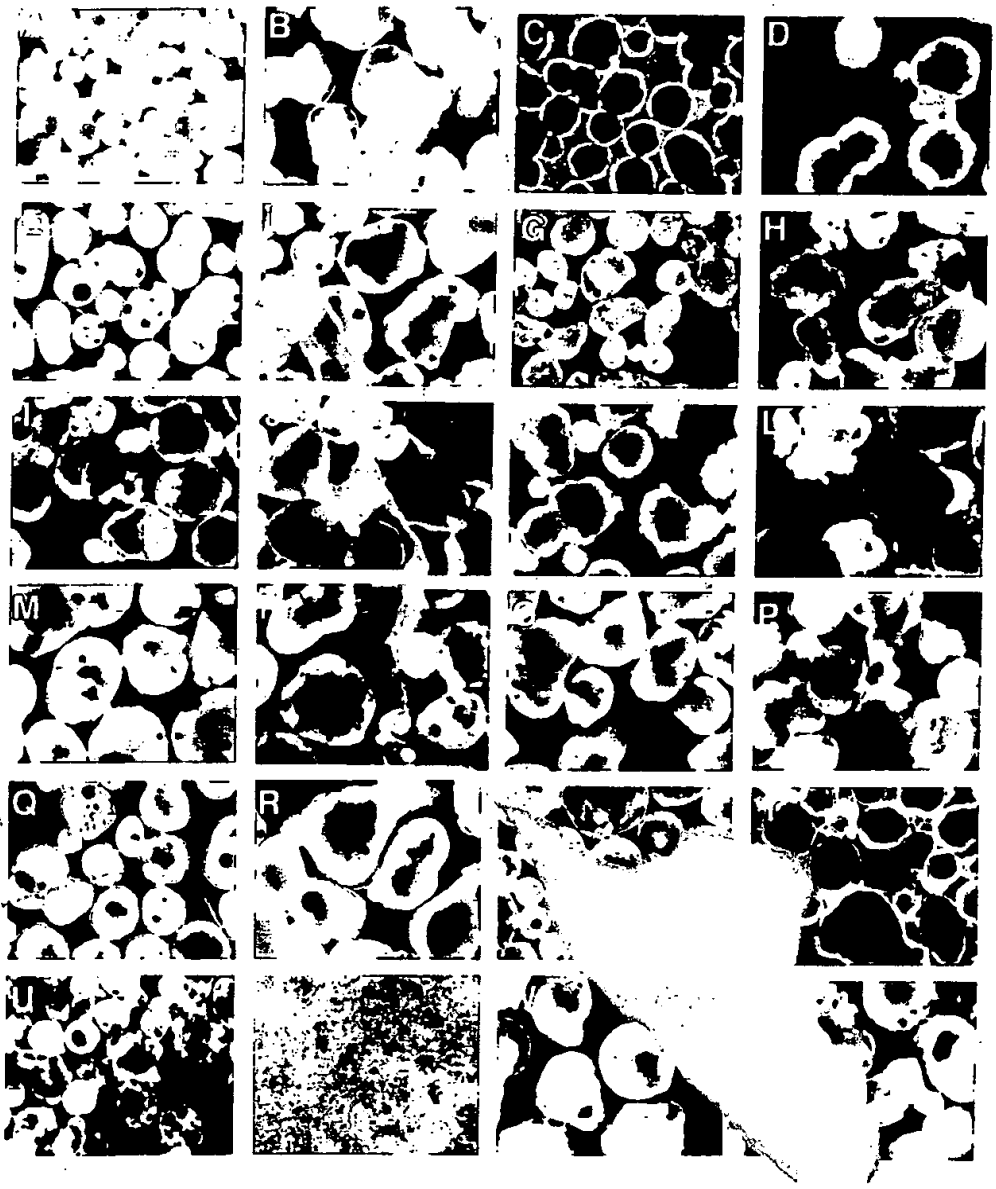
Figure 2 (con't)

```
      1570       1580       1590       1600       1610       1620
CCCAAGCTTTGCCTACATCACCGCCTTGGTAAACAGTATTATAAAATCAAAATATGGGTA
P  Q  A  L  P  T  S  P  P  W  *>

      1630       1640       1650       1660       1670       1680
AAAGTAAATATTTACCAGCAACTTAACTTTTAGTTGATTAAAGCAAAAAGTAAACCATGA

      1690       1700       1710       1720       1730       1740
AATTGGGAGATTTTATTACATTAGTTAATAAGAGTGTGGTAGCATTTTTCTCCAATTTGG

      1750       1760       1770       1780       1790       1800
CTGGGATTATTCAAAGTAGGGTGTGTATGTAACTTATCACTGGACCACTTTAGTTTAATC

      1810       1820       1830       1840       1850       1860
AGAAATTCCTTTTAGCTGACAACATTGCTTAAACAGGATAGTAGTTGGCAAGATGAAATG

      1870       1880       1890       1900       1910       1920
CCAGAATTAAAACCAATCATAAGTAGAACCCACTTCAAAATAAAAAAACAGCATTACTAT

      1930       1940       1950       1960       1970       1980
TTCTAATCCCAAGGAATCACTTTATTGTAAACACTAGCAGAACTCTTCTCCCTATACAAG

      1990       2000       2010       2020       2030       2040
GTGGATGGCTGATTTTAACCTGAAATTTTAAATCCACAGATTGAGAGCTAGTGTAGAATT

      2050       2060       2070       2080       2090       2100
GTCTGTGTTTATTGTTTTTATGAGTAAATACATGCATTGTCATAATAAAATGCATTTCAG

      2110       2120       2130       2140       2150       2160
AGAATATGCATTTTACCTTTGGGAATATGTTAATTTCAGGCAGCATTCCCTATGGGAAAG

      2170       2180       2190       2200       2210       2220
GTGATACCAGCTCTGATATGCAAAGCATATGATAATTTATCATTCTAACTTCAACGTATA

      2230       2240       2250       2260       2270       2280
ATAGGGATTGTGACCTGATATTTGGAGATGTAAATATTGCTCAGCATATTAATCCCGATG

      2290       2300
GAATATAGCATTGTAGTTGACTTTTT
```

Figur 3


A. Retroviral Entrapment Vector
LTR
supF
EcoRI
AP
PGK
neo
LTR
supF
B. Infection of ES cells
Isolation of G418r clones
C. Screen for AP expression in embryoid bodies
Undifferentiated ES cells
Embryoid bodies
Terminally differentiated embryoid bodies
D. Selection of ES cell clones with differential AP expression in vitro
E. Aggregation chimeras
Transfer into pseudo-pregnant foster females
G. Cloning of flanking cellular DNA by supF complementation
F. AP expression in day-8.5 to 9.5 embryos

Figur 4



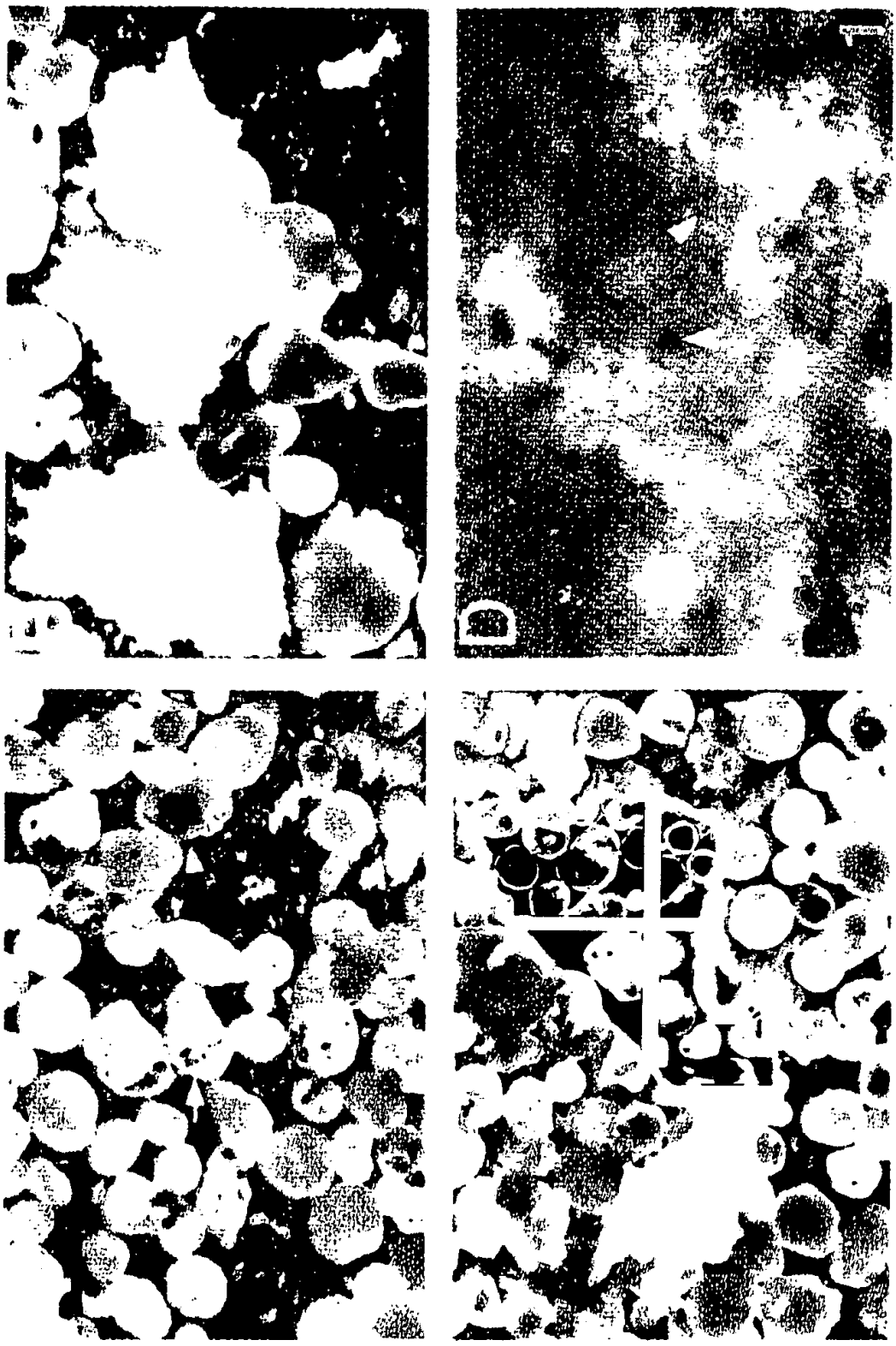
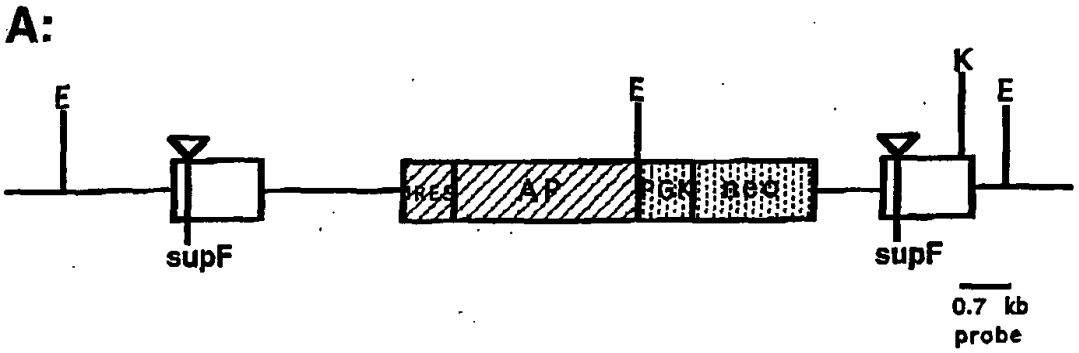
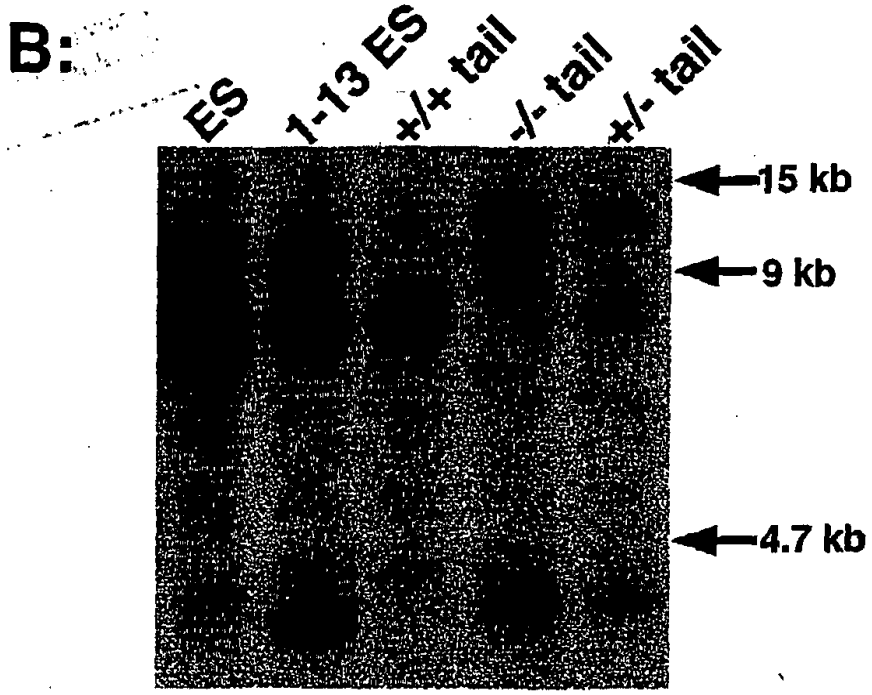


Figure 5

Figure 6


A:
E
E
K
E
supF
supF
0.7 kb
probe


B:
ES
1-13 ES
+/+ tail
-/- tail
+/- tail
15 kb
9 kb
4.7 kb

Alignment of Vezf1/mPur1:

```
Vezf1    168  KPVKKNHACEMCGKAFRDVYHLNRHKLSHSDEKPFECPICNQRFKRKDRMTYHVRSHEGGITKPYTCSVCGKGFSRPDHLSCHVKHVHSTERPFKCQ  264
mPur1    275  KRIRKNHACEMCGKAFRDVYHLNRHKLSHSDEKPYQCPVCQQRFKRKDRMSYHVRSHDGAVHKPYNCSHCGKSFSRPDHLNSHVRQVHSTERPFKCE  372

Vezf1    265  TCTAAPATKDRLRTHMVRHEGKVSCNICGKLLSAAYITSHLKTHGQSQSINCNTCKQGISKTCMSEETSNQKQQQQQQQQQQQQQQQHVTSWPGKQ  360
mPur1    373  KCEAAPATKDRLRAHTVRHEEKVPCHVCGKMLSSAYISDHMKVHSQGPHHVCELCNKGTGEVCPMAAAAAAAAAAAAAAVVAAPPTAVGSLSGAGEV  469
```

Figure 7

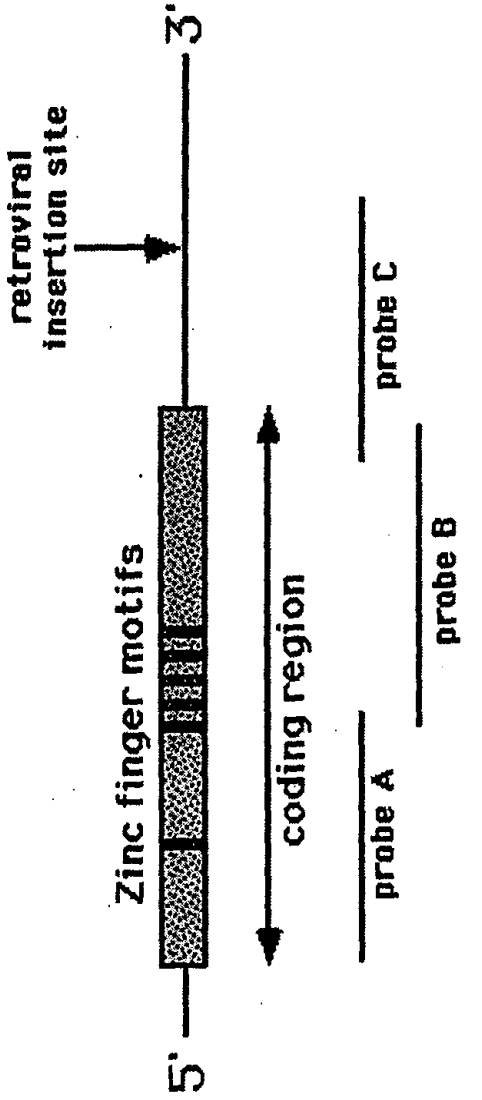

3'
retroviral
insertion site
Zinc finger motifs
coding region
probe C
probe B
probe A
5'

Figure 8

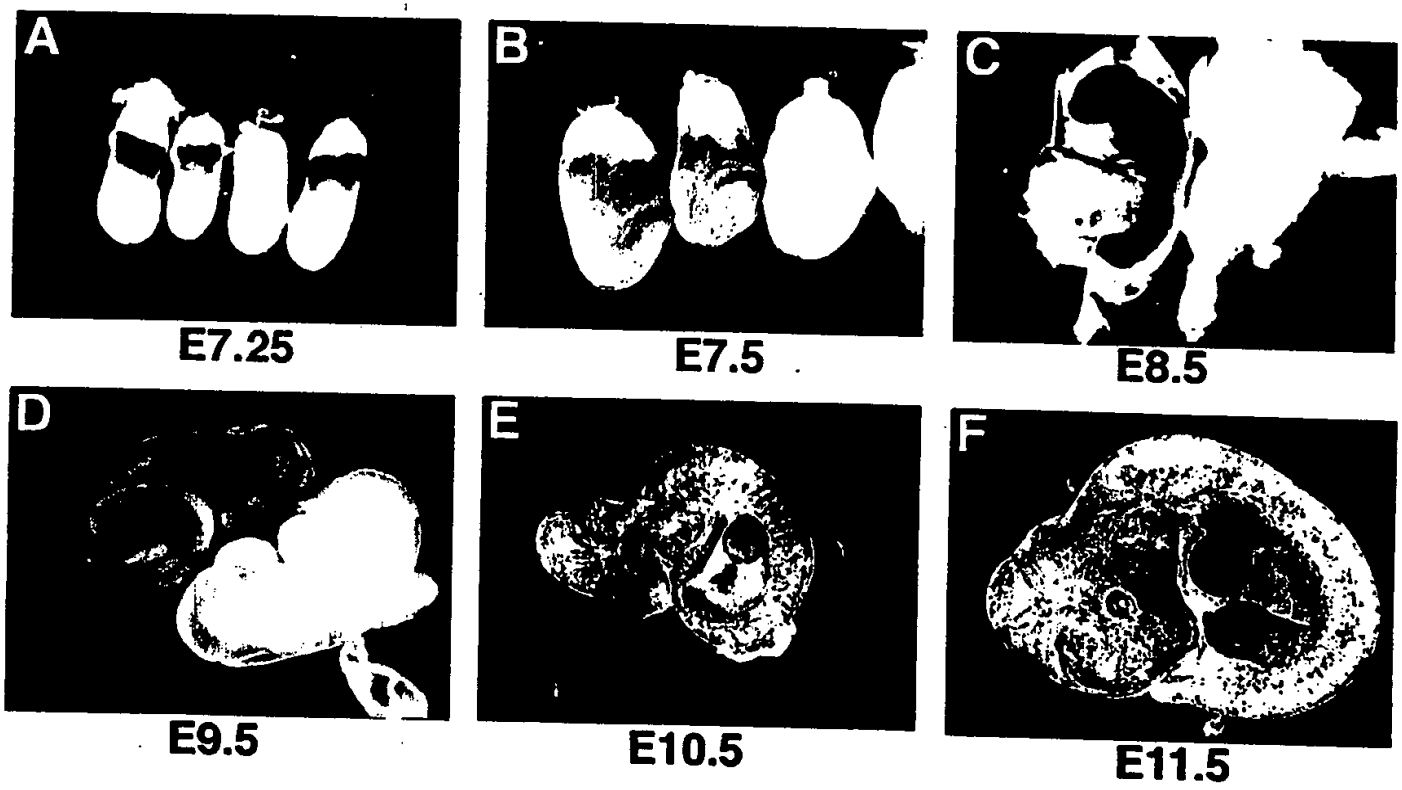


Figure 9

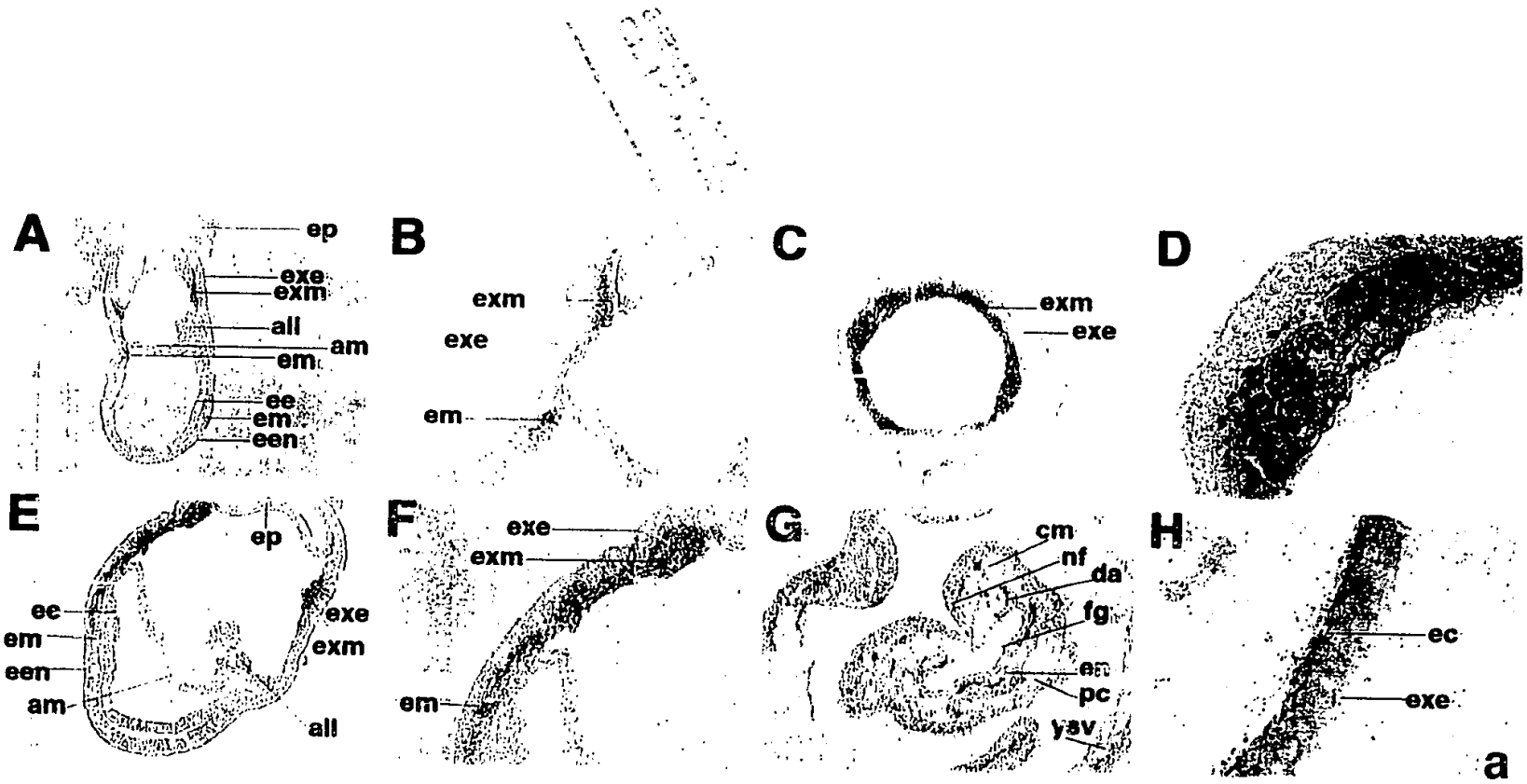
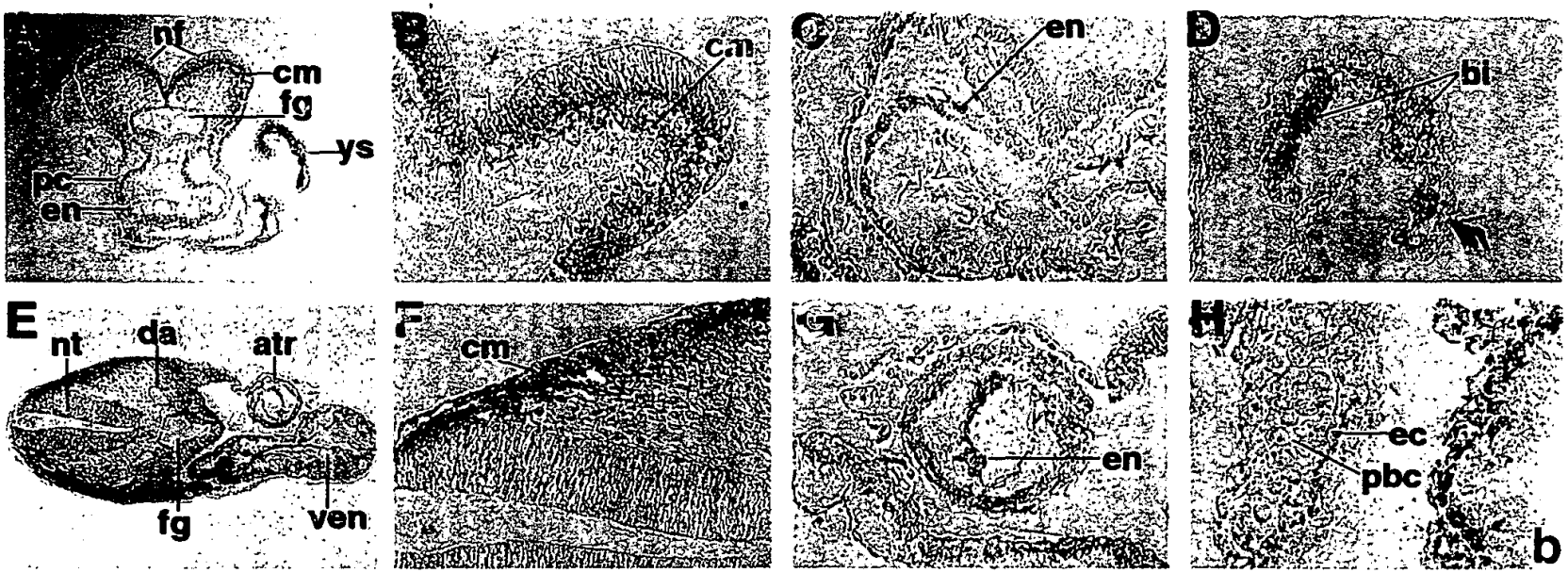

A
ep
exe
exm
all
am
em
ee
em
een
B
exm
exe
em
C
exm
exe
D
E
ep
ee
em
een
am
exe
exm
all
F
exe
exm
em
G
cm
nf
da
fg
en
pc
ysv
H
ec
exe
a

Figure 10

Figure 11



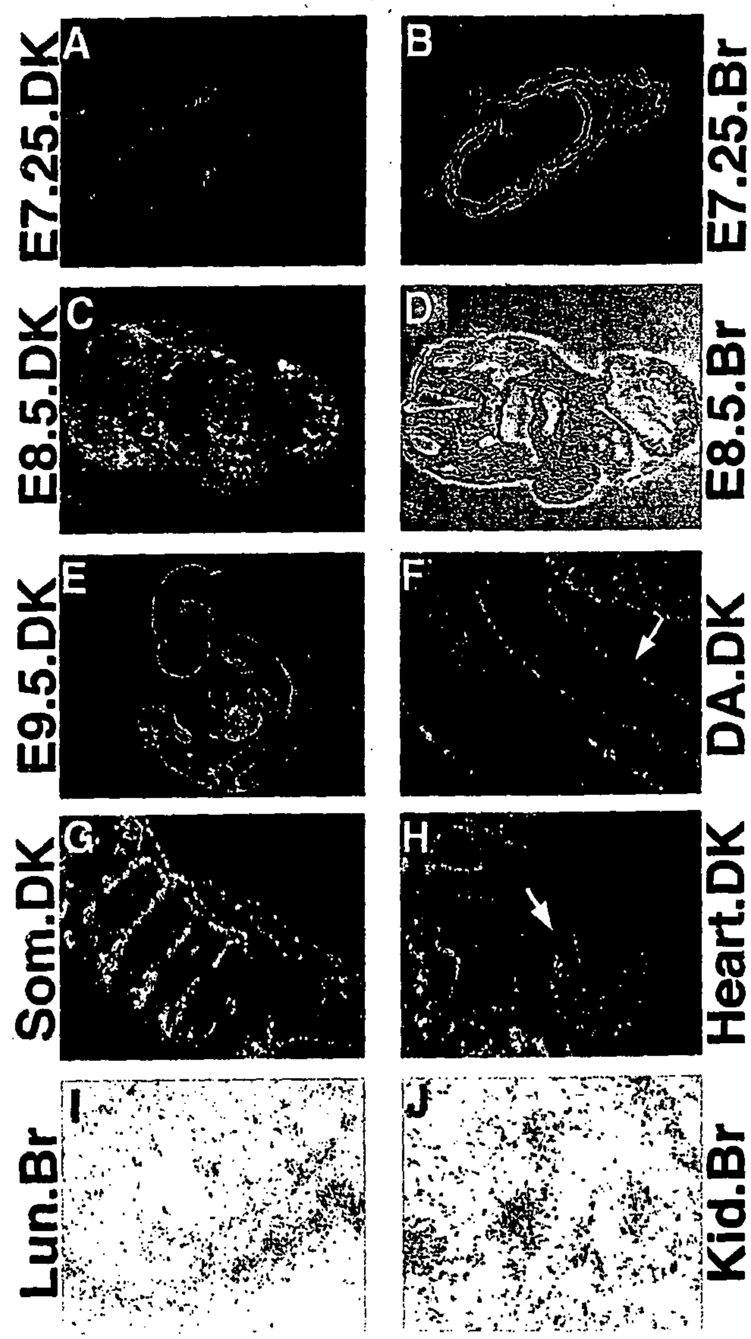
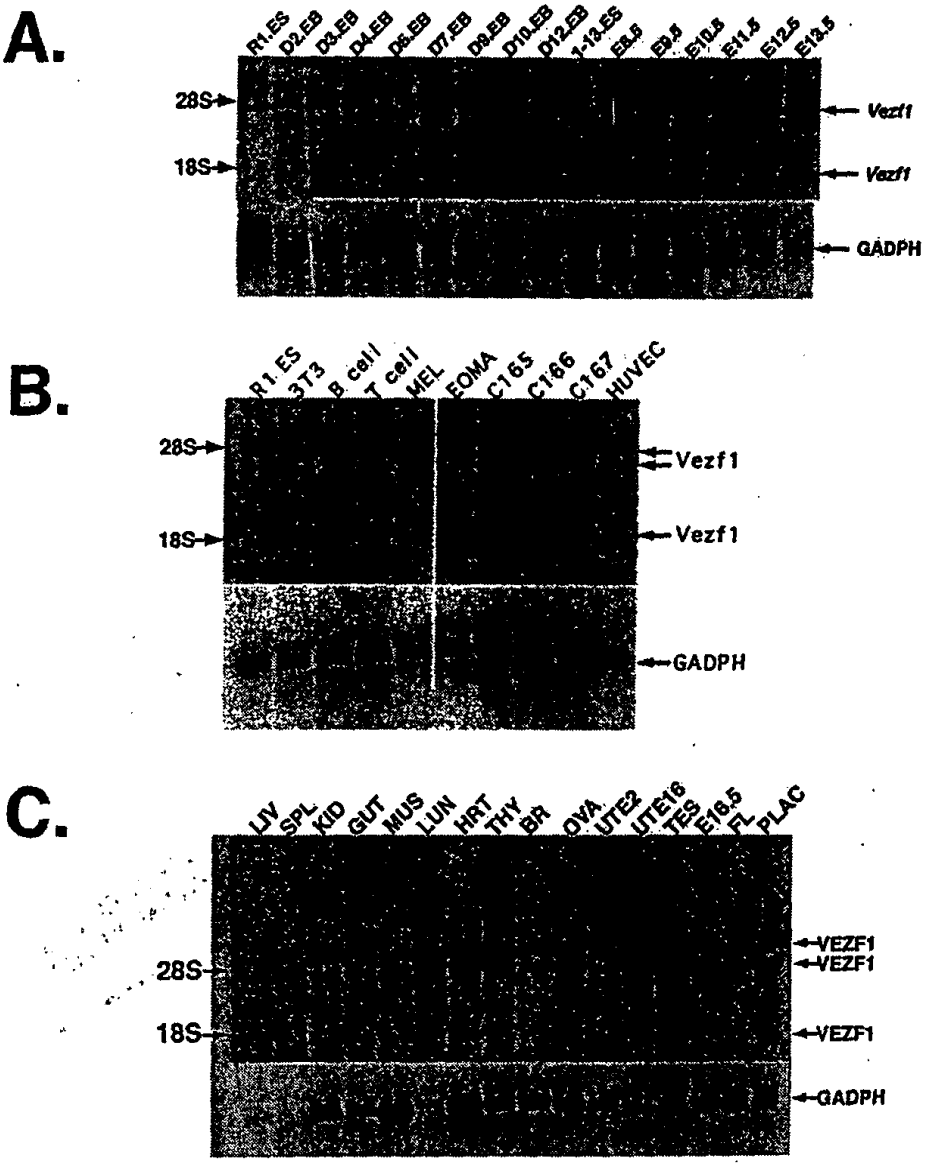

A
E7.25.DK
B
E7.25.Br
C
E8.5.DK
D
E8.5.Br
E
E9.5.DK
F
DA.DK
G
Som.DK
H
Heart.DK
I
Lun.Br
J
Kid.Br

Figure 12

Figure 13


A.
R1.ES
D2.EB
D3.EB
D4.EB
D6.EB
D7.EB
D9.EB
D10.EB
D12.EB
E8.5
E9.5
E10.5
E11.5
E12.5
E13.5
28S
18S
Vezf1
Vezf1
GADPH
B.
R1.ES
3T3
B cell
T cell
MEL
EOMA
C165
C166
C167
HUVEC
28S
18S
Vezf1
Vezf1
GADPH
C.
LIV
SPL
KID
GUT
MUS
LUN
HRT
THY
BR
OVA
UTE2
UTE16
TES
E16.5
FL
PLAC
28S
18S
VEZF1
VEZF1
VEZF1
GADPH

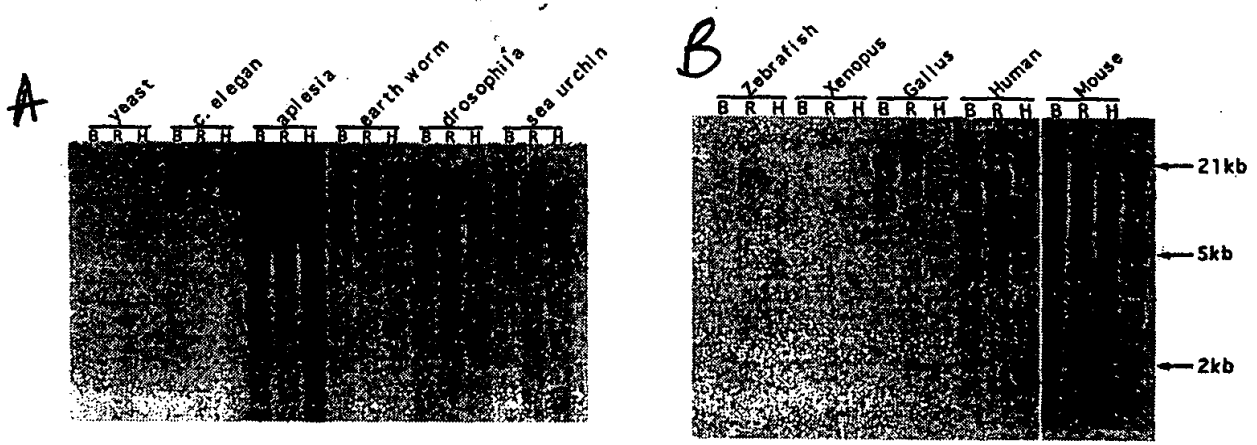
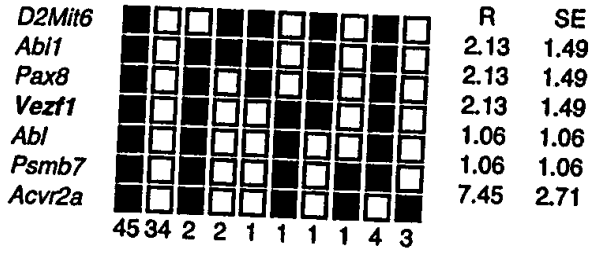

A
yeast
C. elegan
Aplesia
earth worm
drosophila
sea urchin
B R H
B
Zebrafish
Xenopus
Gallus
Human
Mouse
21kb
5kb
2kb

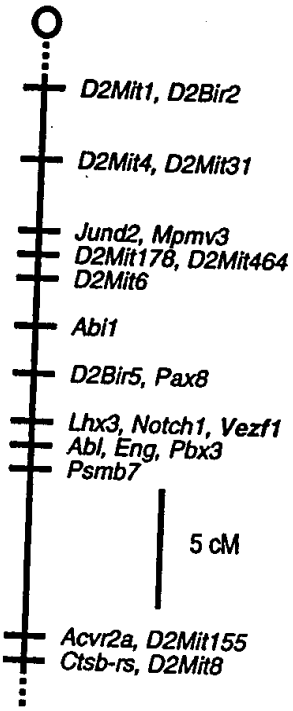
Figure 14

Figur 15

A: Jackson BSS Chromosome 2

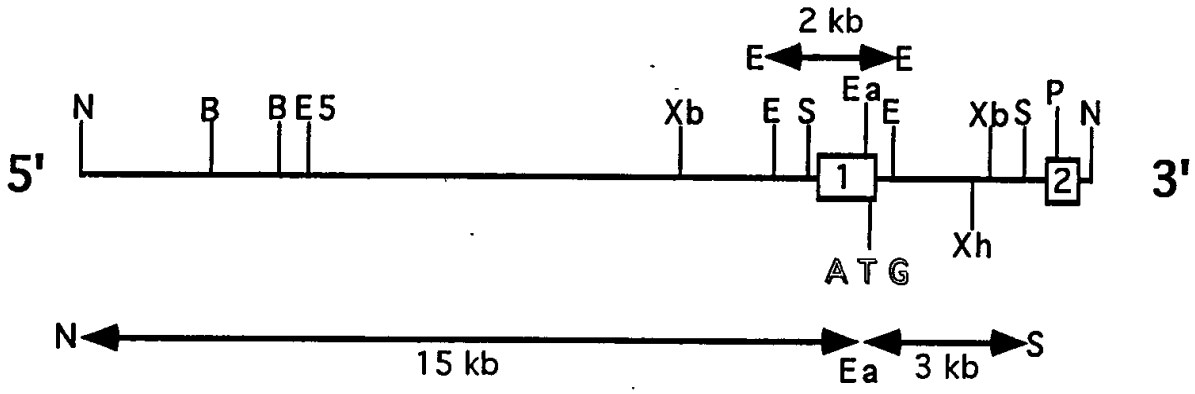


B: Jackson BSS Chromosome 2



Figur 16

Restriction Enzyme Map of a 20 kb Genomic DNA of the Vezf1 Gene



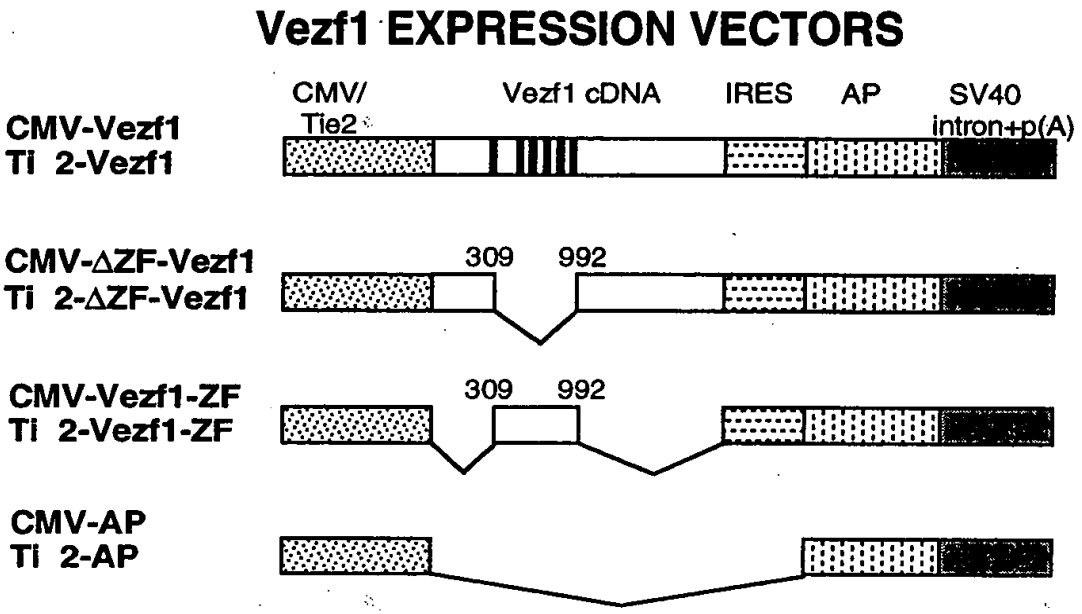
BamHI (B), EcoRI (E), EcoRV (E5), EagI (Ea), NotI (N), PatI (P), SacI (S), XbaI (Xb), and XhoI (Xh).

— Intronic sequence;

1 Exon 1

2 Exon 2

Figure 17


Vezf1 EXPRESSION VECTORS
CMV/
Tie2
Vezf1 cDNA
IRES
AP
SV40
intron+p(A)
CMV-Vezf1
Ti 2-Vezf1
CMV-ΔZF-Vezf1
Ti 2-ΔZF-Vezf1
309
992
CMV-Vezf1-ZF
Ti 2-Vezf1-ZF
309
992
CMV-AP
Ti 2-AP

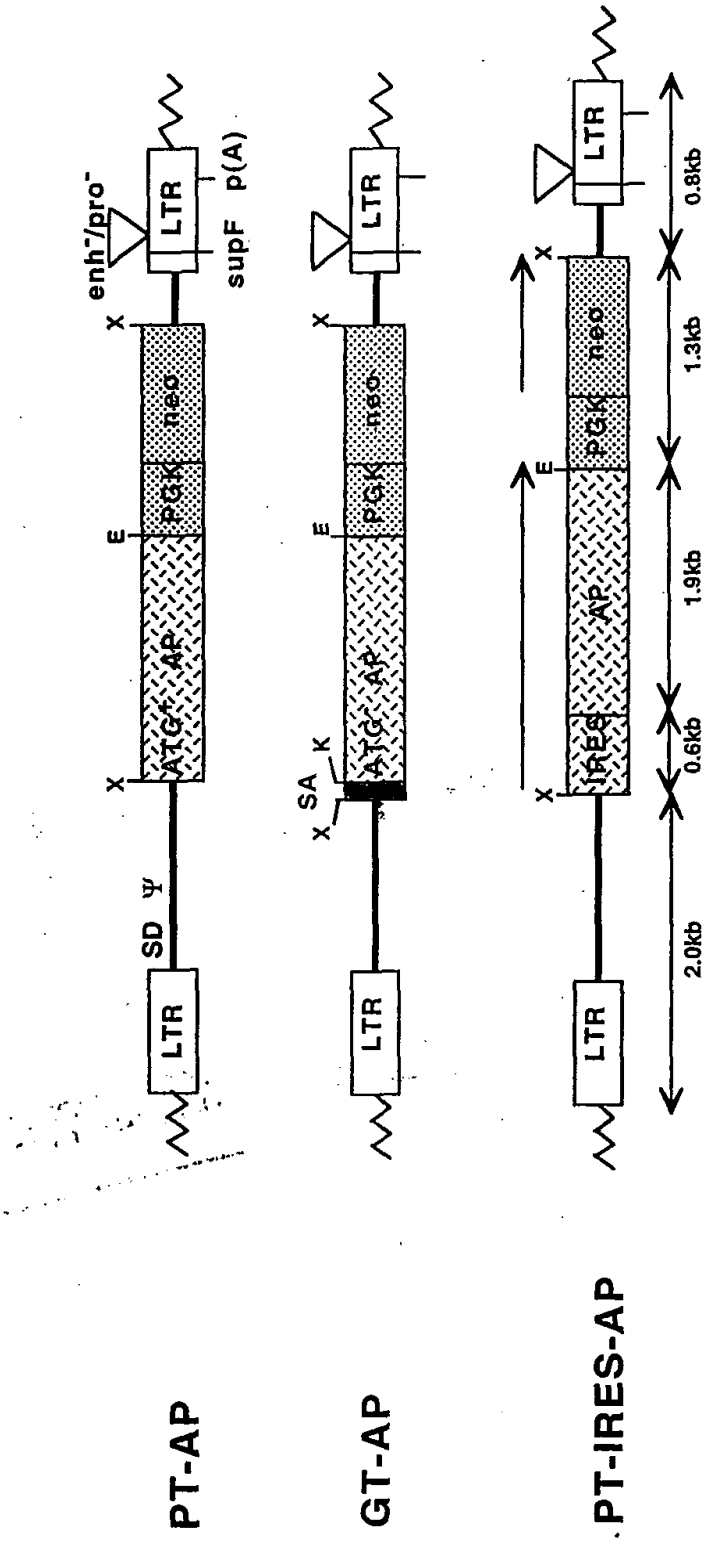

PT-AP
enh-/pro-
LTR
supF
p(A)
X
E
PGK
neo
ATG
AP
X
SD
Ψ
LTR
GT-AP
LTR
X
E
PGK
neo
K
SA
X
ATG
AP
LTR
PT-IRES-AP
LTR
X
E
PGK
neo
X
IRES
AP
LTR
0.8kb
1.3kb
1.9kb
0.6kb
2.0kb

Figure 18